SEQUENCE LISTING

<110> Melbourne Health
     Jane, Stephen (US Only)
     Wilanowski, Tomasz (US only)
     Ting, Stephen (US only)

<120> MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS

<130> DAVI251.001APC

<140> US 10/524,619
<141> 2005-02-09

<150> PCT/AU03/01006
<151> 2003-08-08

<150> US 60/402055
<151> 2002-08-09

<150> AU2002951579
<151> 2002-08-22

<160> 46

<170> PatentIn version 3.1

<210> 1
<211> 1881
<212> DNA
<213> human

<220>
<221> CDS
<222> (94)..(1323)

<400> 1
ataagagagg ccatctgaca gctccagata cgacagtcac tgtctccata gcaacgatgc   60

ctacccactc catcaagaca gaaacccagc cac atg gct tcg ctg tgg gaa tcc   114
                                            Met Ala Ser Leu Trp Glu Ser
                                        1   5

ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg   162
Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser
          10   15   20

atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa   210
Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln
      25   30   35

atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg   258
Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg
40   45   50   55

aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa   306
Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys
                   60   65   70

tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa   354
Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys
          75   80   85

Page 1

```
ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga      402
Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly
        90              95              100

atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt      450
Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe
    105             110             115

gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg      498
Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp
120             125             130             135

cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac      546
His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp
                140             145             150

tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat      594
Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr
            155             160             165

aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc      642
Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe
        170             175             180

atc tct gtg aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg      690
Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
    185             190             195

aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac      738
Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn
200             205             210             215

cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc      786
Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe
            220             225             230

tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa      834
Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
            235             240             245

agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac      882
Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His
            250             255             260

aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act      930
Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr
        265             270             275

cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg      978
Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg
280             285             290             295

ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc     1026
Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly
                300             305             310

tct gtc ttg aaa agg ggg ccg tac ggc aca gaa gat gac ttt gct gtc     1074
Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val
            315             320             325

cct cct tct acc aag ctg gcc cgg ata gaa gaa cca aag aga gtg ctg     1122
Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro Lys Arg Val Leu
```

```
                 330                      335                        340
ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc        1170
Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
    345                      350                        355

aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac        1218
Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
360                      365                        370                375

gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag        1266
Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
                     380                      385                        390

ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat        1314
Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
                 395                      400                        405

gag gac acc ttccagctgc agattgaaga agccgggggg tcttacaagc               1363
Glu Asp Thr
        410

tcaccctgac ggagatctaa aggcctgcgg gccacagctc cccaggagtt cagtgcaggt    1423

gtttctagat cttacggttt ggcaactgca ggtaacccca gtcagccatg tcgccagcac    1483

aggtctatgt cgagggaatg ggttccttgc aggttggagg cggggctgca tctggcttgg    1543

tggtagcatt taatctattg cattggtgtt tttcagatga aagagaaatc catataccat    1603

tatgtttgaa tttcctgata tatacaggat ttaaagtgaa aactttattc caagagttaa    1663

cagagtctct gggaagcttt aggacatctg ctacgttatt tatcaaaata ttgggatctc    1723

tgccttgtgc ctacagtgtc gtgggcctgc tcgctagcag aagtcagaaa aggcgatagg    1783

cttggcttta aggatttcgt gcccttgcct gaattcagta caactccact gcctcacgtt    1843

agcgggagcg cacctgaaga gtacgggggg agccctct                            1881
```

```
<210>   2
<211>   410
<212>   PRT
<213>   human

<400>   2

Met Ala Ser Leu Trp Glu Ser Pro Gln Gln Cys Ile Ile Leu Ser Pro
1               5                   10                  15


Leu Ser Gly Trp Trp Phe Ser Ile Gly Ile Ser Ile Leu Thr Ser Ser
            20                  25                  30


Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
            35                  40                  45


Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
        50                  55                  60
```

Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
65   70   75   80

Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
                85   90   95

Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
            100   105   110

Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
        115   120   125

Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
    130   135   140

Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
145   150   155   160

Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
            165   170   175

Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
            180   185   190

Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
    195   200   205

Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
    210   215   220

Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
225   230   235   240

Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
            245   250   255

Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
            260   265   270

Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
            275   280   285

His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
    290   295   300

Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
305   310   315   320

```
Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
              325             330                 335


Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
              340             345                 350


Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
              355             360                 365


Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
    370             375             380


Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn
385             390             395                 400


Ile Val Lys His Tyr Ser Asn Glu Asp Thr
            405             410
```

```
<210>  3
<211>  2361
<212>  DNA
<213>  human

<220>
<221>  CDS
<222>  (7)..(1860)

<220>
<221>  VARIANT
<222>  342
<223>  Xaa = Lys, Ile


<400>  3
agcgcg atg aca cag gag tac gac aac aaa cgg cca gtg ttg gtt ctt        48
       Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu
       1               5                   10

cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat      96
Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp
15              20                  25                  30

gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa     144
Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys
                35                  40                  45

gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc     192
Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly
            50                  55                  60

ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca     240
Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr
        65                  70                  75

gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac     288
```

```
Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn
    80              85              90

agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac      336
Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn
95              100             105             110

aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat      384
Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His
            115             120             125

ggc aac cag ctg ggc att gat aag aga ggc cat ctg aca gct tca gat      432
Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp
            130             135             140

acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag      480
Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys
            145             150             155

aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg      528
Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val
    160             165             170

tat cat cct gag ccc act gag cgg gtg gtg gtt ttc gat cgg aay ctc      576
Tyr His Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu
175             180             185             190

aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg      624
Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg
            195             200             205

cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag      672
Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln
            210             215             220

gag gtt ttc ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat      720
Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn
        225             230             235

tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat      768
Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr
    240             245             250

acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc      816
Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr
255             260             265             270

atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag      864
Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu
            275             280             285

gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt      912
Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser
            290             295             300

gtg atc atg gtg gtt ttt gct gaa gac aaa agc aga gaa gat cag tta      960
Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu
            305             310             315

agg cat tgg aag tac tgg cac tcc cgg cag cac acc gct aaa caa aga     1008
Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg
    320             325             330
```

```
tgc att gac ata gct gac tat awa gaa agc ttc aac act atc agt aac      1056
Cys Ile Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn
335             340             345                 350

atc gag gag att gcg tat aac gcc att tcc ttc aca tgg gac atc aac  ·   1104
Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn
                355             360                 365

gat gaa gca aag gtt ttc atc tct gtg aac tgc tta agc aca gat ttc      1152
Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe
                370             375                 380

tct tcc cag aag gga gtg aag ggg ttg cct ctt aac att caa gtt gat      1200
Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp
        385             390                 395

acc tat agt tac aac aac cgc agc aac aag cct gtg cac cgg gcc tac      1248
Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr
        400             405                 410

tgc cag atc aag gtc ttc tgt gac aag gga gct gag cgg aaa atc agg      1296
Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg
415             420             425                 430

gat gaa gaa cga aag caa agc aaa aga aaa gtt tct gat gtt aaa gtg      1344
Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val
                435             440                 445

cca ctg ctt ccc tct cac aag cga atg gat atc aca gtt ttc aaa ccc      1392
Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro
                450             455                 460

ttc att gat ctc gat act cag cct gtc ctc ttc att cct gac gtg cac      1440
Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His
                465             470                 475  ·

ttt gcc aac ttg cag cgg ggc act cat gtc ctt ccc att gcc tct gaa      1488
Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu
        480             485                 490

gaa ttg gag ggt gaa ggc tct gtc ttg aaa agg ggg ccg tac ggc aca      1536
Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr
495             500             505                 510

gaa gat gac ttt gct gtc cct cct tct acc aag ctg gcc cgg ata gaa      1584
Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu
                515             520                 525

gaa cca aag aga gtg ctg ctc tac gtt cga aag gag tca gaa gaa gtc      1632
Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val
                530             535                 540

ttt gat gcc ctg atg ctc aaa acc cca tct ttg aag ggc ttg atg gaa      1680
Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu
                545             550                 555

gct atc tca gac aaa tac gat gtt ccc cat gac aag att ggg aaa ata      1728
Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile
        560             565                 570

ttc aag aag tgt aaa aag ggg atc ctg gtg aac atg gac gac aac att      1776
Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile
575             580             585                 590
```

```
gtg aag cat tac tcc aat gag gac acc ttc cag ctg cag att gaa gaa    1824
Val Lys His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu
                595             600             605

gcc ggg ggg tct tac aag ctc acc ctg acg gag atc taaaggcctg         1870
Ala Gly Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
            610             615

cgggccacag ctccccagga gttcagtgca ggtgtttcta gatcttacgg tttggcaact   1930

gcaggtaacc ccagtcagcc atgtcgccag cacaggtcta tgtcgaggga atgggttcct   1990

tgcaggttgg aggcggggct gcatctggct tggtggtagc atttaatcta ttgcattggt   2050

gtttttcaga tgaaagagaa atccatatac cattatgttt gaatttcctg atatatacag   2110

gatttaaagt gaaaacttta ttccaagagt taacagagtc tctgggaagc tttaggacat   2170

ctgctacgtt atttatcaaa atattgggat ctctgccttg tgcctacagt gtcgtgggcc   2230

tgctcgctag cagaagtcag aaaaggcgat aggcttggct ttaaggattt cgtgcccttg   2290

cctgaattca gtacaactcc actgcctcac gttagcggga gcgcacctga agagtacggg   2350

gggagccctc t                                                       2361


<210>   4
<211>   618
<212>   PRT
<213>   human

<220>
<221>   misc_feature
<222>   (342)..(342)
<223>   The 'Xaa' at location 342 stands for Lys, or Ile.

<400>   4

Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn
1               5                   10                  15


Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
                20                  25                  30


Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
            35                  40                  45


Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
        50                  55                  60


Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys
65                  70                  75                  80


Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn Ser Ile
                85                  90                  95
```

Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
         100   105   110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Gly Asn
         115   .120   125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp Thr Thr
         130   135   140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145   150   155   160

Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
         165   170   175

Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu Asn Thr
         180   185   190

Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg Arg Thr
         195   200   205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
         210   215   220

Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
225   230   235   240

Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
         245   250   255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr
         260   265   270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser
         275   280   285

Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
         290   295   300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305   310   315   320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
         325   330   335

Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
         340   345   350

```
Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
        355             360             365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
    370             375             380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr
385             390             395             400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
            405             410             415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
        420             425             430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu
        435             440             445

Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile
    450             455             460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala
465             470             475             480

Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu
            485             490             495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp
            500             505             510

Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro
        515             520             525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
    530             535             540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
545             550             555             560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
            565             570             575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
        580             585             590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
```

```
                595                      600                   605
```

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
   610   615

<210> 5
<211> 4532
<212> DNA
<213> human

<220>
<221> CDS
<222> (67)..(1941)

<400> 5
ttgaaagtcc agtttcacca gaggctgagg ctccaggaaa aggggagcaa gttcattgga   60

tcaaac atg tca caa gag tca gac aat aat aaa aga cta gtg gcc tta   108
       Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu
         1   5   10

gtg ccc atg ccc agt gac cct cca ttc aat acc cga aga gcc tac acc   156
Val Pro Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr
15   20   25   30

agt gag gat gaa gcc tgg aag tca tac ttg gag aat ccc ctg aca gca   204
Ser Glu Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala
                35   40   45

gcc acc aag gcc atg atg agc att aat ggt gat gag gac agt gct gct   252
Ala Thr Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala
                50   55   60

gcc ctc ggc ctg ctc tat gac tac tac aag gtt cct cga gac aag agg   300
Ala Leu Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg
            65   70   75

ctg ctg tct gta agc aaa gca agt gac agc caa gaa gac cag gag aaa   348
Leu Leu Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys
    80   85   90

aga aac tgc ctt ggc acc agt gaa gcc cag agt aat ttg agt gga gga   396
Arg Asn Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly
95   100   105   110

gaa aac cga gtg caa gtc cta aag act gtt cca gtg aac ctt tcc cta   444
Glu Asn Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu
                115   120   125

aat caa gat cac ctg gag aat tcc aag cgg gaa cag tac agc atc agc   492
Asn Gln Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser
                130   135   140

ttc ccc gag agc tct gcc atc atc ccg gtg tcg gga atc acg gtg gtg   540
Phe Pro Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val
                145   150   155

aaa gct gaa gat ttc aca cca gtt ttc atg gcc cca cct gtg cac tat   588
Lys Ala Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr
        160   165   170
```

```
ccc cgg gga gat ggg gaa gag caa cga gtg gtt atc ttt gaa cag act    636
Pro Arg Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr
175             180             185                 190

cag tat gac gtg ccc tcg ctg gcc acc cac agc gcc tat ctc aaa gac    684
Gln Tyr Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp
            195             200             205

gac cag cgc agc act ccg gac agc aca tac agc gag agc ttc aag gac    732
Asp Gln Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp
                210             215             220

gca gcc aca gag aaa ttt cgg agt gct tca gtt ggg gct gag gag tac    780
Ala Ala Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr
        225             230             235

atg tat gat cag aca tca agt ggc aca ttt cag tac acc ctg gaa gcc    828
Met Tyr Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala
    240             245             250

acc aaa tct ctc cgt cag aag cag ggg gag ggc ccc atg acc tac ctc    876
Thr Lys Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu
255             260             265             270

aac aaa gga cag ttc tat gcc ata aca ctc agc gag acc gga gac aac    924
Asn Lys Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn
                275             280             285

aaa tgc ttc cga cac ccc atc agc aaa gtc agg agt gtg gtg atg gtg    972
Lys Cys Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val
            290             295             300

gtc ttc agt gaa gac aaa aac aga gat gaa cag ctc aaa tac tgg aaa   1020
Val Phe Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys
        305             310             315

tac tgg cac tct cgg cag cat acg gcg aag cag agg gtc ctt gac att   1068
Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile
    320             325             330

gcc gat tac aag gag agc ttt aat acg att gga aac att gaa gag att   1116
Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile
335             340             345             350

gca tat aat gct gtt tcc ttt acc tgg gac gtg aat gaa gag gcg aag   1164
Ala Tyr Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys
                355             360             365

att ttc atc acc gtg aat tgc ttg agc aca gat ttc tcc tcc caa aaa   1212
Ile Phe Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
            370             375             380

ggg gtg aaa gga ctt cct ttg atg att cag att gac aca tac agt tat   1260
Gly Val Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr
        385             390             395

aac aat cgt agc aat aaa ccc att cat aga gct tat tgc cag atc aag   1308
Asn Asn Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys
    400             405             410

gtc ttc tgt gac aaa gga gca gaa aga aaa atc cga gat gaa gag cgg   1356
Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
```

<pre>
415   420   425   430

aag cag aac agg aag aaa ggg aaa ggc cag gcc tcc caa act caa tgc   1404
Lys Gln Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys
            435   440   445

aac agc tcc tct gat ggg aag ttg gct gcc ata cct tta cag aag aag   1452
Asn Ser Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys
            450   455   460

agt gac atc acc tac ttc aaa acc atg cct gat ctc cac tca cag cca   1500
Ser Asp Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro
            465   470   475

gtt ctc ttc ata cct gat gtt cac ttt gca aac ctg cag agg acc gga   1548
Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly
    480   485   490

cag gtg tat tac aac acg gat gat gaa cga gaa ggt ggc agt gtc ctt   1596
Gln Val Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu
495   500   505   510

gtt aaa cgg atg ttc cgg ccc atg gaa gag gag ttt ggt cca gtg cct   1644
Val Lys Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro
                515   520   525

tca aag cag atg aaa gaa gaa ggg aca aag cga gtg ctc ttg tac gtg   1692
Ser Lys Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val
                530   535   540

agg aag gag act gac gat gtg ttc gat gca ttg atg ttg aag tct ccc   1740
Arg Lys Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro
            545   550   555

aca gtg aag ggc ctg atg gaa gcg ata tct gag aaa tat ggg ctg ccc   1788
Thr Val Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro
    560   565   570

gtg gag aag ata gca aag ctt tac aag aaa agc aaa aaa ggc atc ttg   1836
Val Glu Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu
575   580   585   590

gtg aac atg gat gac aac atc atc gag cac tac tcg aac gag gac acc   1884
Val Asn Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr
                595   600   605

ttc atc ctc aac atg gag agc atg gtg gag ggc ttc aag gtc acg ctc   1932
Phe Ile Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu
                610   615   620

atg gaa atc tagccctggg tttggcatcc gctttggctg gagctctcag   1981
Met Glu Ile
            625

tgcgttcctc cctgagagag acagaagccc cagccccaga acctggagac ccatctcccc   2041

catctcacaa ctgctgttac aagaccgtgc tggggagtgg ggcaagggac aggccccact   2101

gtcggtgtgc ttggcccatc cactggcacc taccacggag ctgaagcctg agcccctcag   2161

gaaggtgcct taggcctgtt ggattcctat ttattgccca ccttttcctg gagcccaggt   2221

ccaggcccgc caggactctg caggtcactg ctagctccag atgagaccgt ccagcgttcc   2281
</pre>

```
cccttcaaga gaaacactca tcccgaacag cctaaaaaat tcccatccct tctctctcac   2341

ccctccatat ctatctcccg agtggctgga caaaatgagc tacgtctggg tgcagtagtt   2401

ataggtgggg caagaggtgg atgcccactt tctggtcaga cacctttagg ttgctctggg   2461

gaaggctgtc ttgctaaata cctccagggt tcccagcaag tggccaccag gccttgtaca   2521

ggaagacatt cagtcaccgt gtaattagta acacagaaag tctgcctgtc tgcattgtac   2581

atagtgttta taatattgta ataatatatt ttacctgtgg tatgtgggca tgtttactgc   2641

cactggcctt agaggagaca cagacctgga gaccgtttta atggggggtttt ttgcctctgt   2701

gcctgttcaa gagacttgca gggctaggta gagggccttt gggatgttaa ggtgactgca   2761

gctgatgcca agatggactc tgcaatgggc atacctgggg gctcgttccc tgtccccaga   2821

ggaagccccc tctccttctc catgggcatg actctccttc gaggccacca cgtttatctc   2881

acaatgatgt gttttgcttg actttccctt tgcgctgtct cgtgggaaag gtcattctgt   2941

ctgagacccc agctccttct ccagctttgg ctgcgggcat ggcctgagct ttctggagag   3001

cctctgcagg gggtttgcca tcagggccct gtggctgggt ctgctgcaga gctccttggc   3061

tatcaggaga atcctggaca ctgtactgtg cctcccagtt tacaaacacg cccttcatct   3121

caagtggccc tttaaaaggc ctgctgccat gtgagagctg tgaacagctc agctctgagt   3181

cggcaggctg gggcttcctc ctgggccacc agatggaaag ggggtattgt ttgcctcact   3241

cctggatgct gcgttttaag gaagtgagtg agaaagaatg tgccaagata cctggctcct   3301

gtgaaaccag cctcaggagg gaaactggga gagagaagct gtggtctcct gctacatgcc   3361

ctgggagctg gaagagaaaa acactcccct aaacaatcgc aaaatgatga accatcatgg   3421

gccactgttc tctttgaggg gacaggttta ggggtttgcg ttcgcccttg tgggctgaag   3481

cactagcttt ttggtagcta gacacatcct gcacccaaag gttctctaca aaggcccaga   3541

tttgtttgta aagcactttg actcttacct ggaggcccgc tctctaaggg cttcctgcgc   3601

tcccacctca tctgtccctg agatgcagag caggatggag ggtctgcttc tagctcagct   3661

gtttctcctt gaggttgcgg aggaattgaa ttgaatggga cagagggcag gtgctgtggc   3721

caagaagatc tccgagcagc agtgacgggg caccttgctg tgtgtcctct gggcatgtta   3781

acccttctgt ggggccaaag gtttgcatcg tggatccagc tgtgctccag tctgtcccct   3841

cctcctccac tctgactgcc acgccccgga ccagcagctt ggggaccctc cagggtacta   3901

atggggctct gttctgagat ggacaaattc agtgttggaa atacatgttg tactatgcac   3961

ttcccatgct cctagggtta ggaatagttt caaacatgat tggcagacat aacaacggca   4021

aatactcgga ctggggcata ggactccaga gtaggaaaaa gacaaaagat ttggcagcct   4081

gacacaggca acctacccct ctctctccag cctctttatg aaactgtttg tttgccagtc   4141
```

```
ctgccctaag gcagaagatg aattgaagat gctgtgcatg tttcctaagt ccttgagcaa    4201

tcatggtggt gacaattgcc acaagggata tgaggccagt gccaccagag ggtggtgcca    4261

agtgccacat cccttccgat ccattcccct ctgcatcctc ggagcacccc agtttgcctt    4321

tgatgtgtcc gctgtgtatg ttagctgaac tttgatgagc aaaatttcct gagcgaaaca    4381

ctccaaagag ataggaaaac ttgccgcctc ttcttttttg tcccttaatc aaactcaaat    4441

aagcttaaaa aaaatccatg gaagatcatg gacatgtgaa atgagcattt ttttcttttt    4501

tttttttttt tttaacaaag tctgaactga g                                  4532
```

<210> 6
<211> 625
<212> PRT
<213> human

<400> 6

```
Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1               5                   10                  15


Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
                20                  25                  30


Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
        35                  40                  45


Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
    50                  55                  60


Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65                  70                  75                  80


Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn
                85                  90                  95


Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn
                100                 105                 110


Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln
            115                 120                 125


Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro
        130                 135                 140


Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145                 150                 155                 160


Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
```
Page 15

                          165   170   175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
            180   185   190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln
        195   200   205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala
    210   215   220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr
225   230   235   240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
            245   250   255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
            260   265   270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
            275   280   285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
    290   295   300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
305   310   315   320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
            325   330   335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
            340   345   350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
            355   360   365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
    370   375   380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385   390   395   400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
            405   410   415

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
        420   425   430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser
        435   440   445

Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
    450   455   460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465   470   475   480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
            485   490   495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys
        500   505   510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys
        515   520   525

Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys
    530   535   540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545   550   555   560

Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu
            565   570   575

Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
        580   585   590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
        595   600   605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu
    610   615   620

Ile
625

<210>   7
<211>   1870
<212>   DNA
<213>   HUMAN

<220>
<221>   CDS

<222>   (47)..(1867)

<220>
<221>   VARIANT
<222>   117
<223>   Xaa = Phe, Leu

<220>
<221>   VARIANT
<222>   172
<223>   Xaa = Thr

<400>   7
aggagatgtg ccaaactgtt aagagtggtt atttctgagc agaaga atg tgg atg   55
                                                      Met Trp Met
                                                       1

aat tcc att ctt cct att ttt ctt ttc agg tct gtg cgg ctg cta aag   103
Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg Leu Leu Lys
 5   10   15

aac gac cca gtc aac ttg cag aaa ttc tct tac act agt gag gat gag   151
Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser Glu Asp Glu
20   25   30   .   35

gcc tgg aag acg tac cta gaa aac ccg ttg aca gct gcc aca aag gcc   199
Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala
                40   45   50

atg atg aga gtc aat gga gat gat gac agt gtt gcg gcc ttg agc ttc   247
Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala Leu Ser Phe
                55   60   65

ctc tat gat tac tac atg ggt ccc aag gag aag cgg ata ttg tcc tcc   295
Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser
            70   75   80

agc act ggg ggc agg aat gac caa gga aag agg tac tac cat ggc atg   343
Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr His Gly Met
    85   90   95

gaa tat gag acg gac ctc act ccc ctt gaa agc ccc aca cac ctc atg   391
Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr His Leu Met
100   105   110   115

aaa ytc ctg aca gag aac gtg tct gga acc cca gag tac cca gat ttg   439
Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr Pro Asp Leu
                120   125   130

ctc aag aag aat aac ctg atg agc ttg gag ggg gcc ttg ccc acc cct   487
Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu Pro Thr Pro
                135   140   145

ggc aag gca gct ccc ctc cct gca ggc ccc agc aag ctg gag gcc ggc   535
Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu Glu Ala Gly
            150   155   160

tct gtg gac agc tac ctg tta ccc acy act gat atg tat gat aat ggc   583
Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr Asp Asn Gly
        165   170   175

```
tcc ctc aac tcc ttg ttt gag agc att cat ggg gtg ccg ccc aca cag     631
Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln
180             185             190             195

cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag gag tcg atg     679
Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Met
            200             205             210

ctc ttc cca gat atc ctg aaa acc tcc ccg gaa ccc cca tgt cca gag     727
Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro Cys Pro Glu
            215             220             225

gac tac ccc agc ctc aaa agt gac ttt gaa tac acc ctg ggc tcc ccc     775
Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro
            230             235             240

aaa gcc atc cac atc aag tca ggc gag tca ccc atg gcc tac ctc aac     823
Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala Tyr Leu Asn
            245             250             255

aaa ggc cag ttc tac ccc gtc acc ctg cgg acc cca gca ggt ggc aaa     871
Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys
260             265             270             275

ggc ctt gcc ttg tcc tcc aac aaa gtc aag agt gtg gtg atg gtt gtc     919
Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val Met Val Val
            280             285             290

ttc gac aat gag aag gtc cca gta gag cag ctg cgc ttc tgg aag cac     967
Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe Trp Lys His
            295             300             305

tgg cat tcc cgg caa ccc act gcc aag cag cgg gtc att gac gtg gct     1015
Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala
            310             315             320

gac tgc aaa gaa aac ttc aac act gtg gag cac att gag gag gtg gcc     1063
Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu Glu Val Ala
            325             330             335

tat aat gca ctg tcc ttt gtg tgg aac gtg aat gaa gag gcc aag gtg     1111
Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val
340             345             350             355

ttc atc ggc gta aac tgt ctg agc aca gac ttt tcc tca caa aag ggg     1159
Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly
                360             365             370

gtg aag ggt gtc ccc ctg aac ctg cag att gac acc tat gac tgt ggc     1207
Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly
            375             380             385

ttg ggc act gag cgc ctg gta cac cgt gct gtc tgc cag atc aag atc     1255
Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile
            390             395             400

ttc tgt gac aag gga gct gag agg aag atg cgc gat gac gag cgg aag     1303
Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys
            405             410             415

cag ttc cgg agg aag gtc aag tgc cct gac tcc agc aac agt ggc gtc     1351
Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Ser Gly Val
```

420   425   430   435

```
aag ggc tgc ctg ctg tcg ggc ttc agg ggc aat gag acg acc tac ctt    1399
Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu
            440                      445                  450

cgg cca gag act gac ctg gag acg cca ccc gtg ctg ttc atc ccc aat    1447
Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe Ile Pro Asn
            455                      460                  465

gtg cac ttc tcc agc ctg cag cgc tct gga ggg gca gcc ccc tcg gca    1495
Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala Pro Ser Ala
            470                      475                  480

gga ccc agc agc tcc aac agg ctg cct ctg aag cgt acc tgc tcg ccc    1543
Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro
            485                      490                  495

ttc act gag gag ttt gag cct ctg ccc tcc aag cag gcc aag gaa ggc    1591
Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly
500                      505                      510                  515

gac ctt cag aga gtt ctg ctg tat gtg cgg agg gag act gag gag gtg    1639
Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val
            520                      525                  530

ttt gac gcg ctc atg ttg aag acc cca gac ctg aag ggg ctg agg aat    1687
Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn
            535                      540                  545

gcg atc tct gag aag tat ggg ttc cct gaa gag aac att tac aaa gtc    1735
Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile Tyr Lys Val
            550                      555                  560

tac aag aaa tgc aag cga gga atc tta gtc aac atg gac aac aac atc    1783
Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile
            565                      570                  575

att cag cat tac agc aac cac gtc gcc ttc ctg ctg gac atg ggg gag    1831
Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu
580                      585                      590                  595

ctg gac ggc aaa att cag atc atc ctt aag gag ctg taa                1870
Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
            600                      605
```

<210> 8
<211> 607
<212> PRT
<213> HUMAN

<220>
<221> misc_feature
<222> (117)..(117)
<223> The 'Xaa' at location 117 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (172)..(172)
<223> The 'Xaa' at location 172 stands for Thr.

<400> 8

```
Met Trp Met Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg
1               5                   10              15

Leu Leu Lys Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser
            20              25              30

Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
        35              40              45

Thr Lys Ala Met Met Arg Val Asn Gly Asp Asp Ser Val Ala Ala
    50              55              60

Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
65              70              75                      80

Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr
            85              90              95

His Gly Met Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr
            100             105             110

His Leu Met Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr
            115             120             125

Pro Asp Leu Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu
    130             135             140

Pro Thr Pro Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu
145             150             155             160

Glu Ala Gly Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr
            165             170             175

Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
            180             185             190

Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
    195             200             205

Glu Ser Met Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro
    210             215             220

Cys Pro Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu
225             230             235             240

Gly Ser Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala
            245             250             255
```

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
            260   265   270

Gly Gly Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val
            275   280   285

Met Val Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe
290   295   300

Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile
305   310   315   320

Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu
            325   330   335

Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu
            340   345   350

Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
            355   360   365

Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
            370   375   380

Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln
385   390   395   400

Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp
            405   410   415

Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn
            420   425   430

Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr
            435   440   445

Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe
    450   455   460

Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala
465   470   475   480

Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr
            485   490   495

Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala

```
              500                  505                  510
```

Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr
        515   520   525

Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly
    530   535   540

Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile
545   550   555   560

Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp
            565   570   575

Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp
        580   585   590

Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
        595   600   605

```
<210>  9
<211>  3113
<212>  DNA
<213>  MURINE

<220>
<221>  misc_feature
<222>  (2634)..(2634)
<223>  n = any nucleotide

<220>
<221>  misc_feature
<222>  (2968)..(2968)
<223>  n = any nucleotide

<400>  9
gttcctccat gggttccttg agttcctgac atggcttccc ttgatgatga actgtgtgac      60
ctaaacagca taccaaatgt gacggagcag cccctcattt ctgctggaga aaacagggta     120
caagtgctga aaaacgtgcc cttcaacatc gtcctccccc atagcaacca gctgggcatt     180
gataagagag gccatctgac agctcccgat acaacagtca ctgtctccat agcgaccatg     240
cctacccact ccatcaagac agaaatccag ccgcacggct ttgctgtggg aatccctcca     300
gccgtgtacc actctgagcc caccgaacgc gtggtggttt ttgaccggag cctcagcact     360
gatcagttca gctctggcac tcagcccccc aatgctcagc ggaggactcc agactccacc     420
ttctccgaga ccttcaagga gggcgttcag gaggttttct tcccctcgga actcagcctt     480
cggatgccgg gcatgaattc agaggactat gtctttgaca atgtttctgg gaacaacttt     540
```

```
gagtataccc tggaagcctc caagtcactg cggcagaagc aaggggacag cactatgaca    600

tacctgaata aaggccagtt ctatcctgtc accttaaagg aaggaagcag caatgaaggg    660

attcaccacc ctatcagcaa agttcgaagt gtgatcatgg tggttttttgc tgaagacaaa   720

agcagagaag accagctgag acactggaag tactggcact cccgtcagca cacggccaaa    780

cagaggtgca ttgacattgc tgactacaaa gaaagtttca acactatcag caacattgag    840

gagatagctt ataacgccat ttccttcacg tgggacatca atgatgaggc aaaggtcttc    900

atctctgtga actgcttgag cacagatttc tcttctcaga agggtgtgaa gggcttgcca    960

ctcaacattc aaatcgacac atacagctat aacaaccgca gcaacaagcc ggttcaccgg    1020

gcctactgcc agataaaggt cttctgcgac aagggagctg aaaggaaaat tcgggatgaa    1080

gaacgaaaac agagcaagag aaaagtgtct gacgttaaag tgcagctgct tccctcacac    1140

aaacggacag acatcacagt gttcaagccc ttcctggacc tcgacactca gcctgtcctc    1200

ttcattccgg acgtgcattt taccaacctg cagcggggca gtcatgttct ttccctcccc    1260

tctgaagaac tggaaggtga aggctctgtc ttgaaaagag ggccattcgg aaccgaagat    1320

gactttggag ttcctcctcc tgctaagctg actcggacag aagaacccaa gagagtgctg    1380

ctctatgtcc gaaaggaatc agaagaagtc ttcgacgccc tgatgctcaa gacgccgtct    1440

ttgaagggcc tgatggaggc aatttcagac aagtatgatg tcccccatga caagattggg    1500

aaaatattta agaagtgcaa aaaagggatc ctcgtgaaca tggacgacaa cattgtgaag    1560

cactactcca atgaggacac cttccagctg cagatagagg aagccggcgg ctcgtacaag    1620

ctcacccctga cagagattta aaggggcagg ggtgggggggc gctcggctcc caggcgtggg   1680

aattcagtga aagtgttcca gctgagaagc ccaggcacct accctgcaga accttaaata    1740

tcagggaagg aacctttcac gtaggaaatg gcgctgtgta taccgtgctg tgttgatgtt    1800

ttctttgga tagaaatcca tgtgttgttt tgttgttgtt gtttgaattt ctgatgtgct     1860

tagaaagcga agcatgagaa ctttgtaccg gatctaagag accatgggac cgtttgggtt    1920

acctgctcca ctacctgtca aagtctgcct gtgtccataa gagtggtggg ctactggctg    1980

gcgagagagg ggaaggcagt agcttgtctt tgaggctttt gtgttctcgc ctgacctcag    2040

tctaactctg actgccttga ggagtgggcc cagccctcag caataaaggg ctaagccttc    2100

tccctccacc tctcctccag tgtttactaa atagggtgca ttcctggaac cttttcccgc    2160

aacttccctt ggacatgtgg actgcctttc tgatgaagaa cttgcgtgag tgacagtgtg    2220

aagttagctc tgttaaagct gcgttgtata taagtgcaat atcttttttga aggtctgcct   2280

gtaaatgtgt acatatatgt ctgatataaa tatataatat ataaatgcgg tgtctgtgta    2340

cagatagtga aggcgagcag gaagatctac cttgaaatcc ctcttagaga agaggttaag    2400

ttattattga taatgtggac caagcaggta gaacgctgtt ttcccaaaaa caagcaagtg     2460
```

```
ttccctagca tagcaaaaag ccatctcatg tggcagagcc atctgctctt gcgaatgttg    2520

tcaccgtgtg ggtttctgca ccctgagtgg agctaatgga agactggact gcagctacta    2580

tatgaggtgt gtgtgcaggt gtcagccaag ctgtgcccat gcagagactc agcngtgtca    2640

tgagccagcg attcaaacca aaatgggccg attctacaag gccatgtttc agagcttcca    2700

agcatcagct accgtgtgtt tgaactggaa ggcattcatg aatttacata actgtggcag    2760

gggaatgttt tgtgcacact aaatatttta agaacaaaac gaaactttac aatgtaaytt    2820

tataatgaat cctgtaacag aaatacaatt gcgggtttct ttaggttcag ggaactagaa    2880

taggtcattt gtatgagtag gattgttagc ggtatacgta rgttaaaaag tactctaatg    2940

aagtatgtga acaaaatagc tggttttnta agatacggga tacgggtcat ataacaatat    3000

tttctatttt gttttatgaa atcagcttta cttgtttttaa ttgtatcatt gaacatgtgt    3060

tttaaaccaa agggattgaa ttttatatgt ctatttcaaa aaaaaaaaaa aaa    3113
```

<210> 10
<211> 536
<212> PRT
<213> MURINE

<400> 1

```
Met Ala Ser Leu Asp Asp Glu Leu Cys Asp Leu Asn Ser Ile Pro Asn
1               5                   10                  15


Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val Gln Val
            20                  25                  30


Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn Gln Leu
        35                  40                  45


Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr Val Thr
    50                  55                  60


Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu Ile Gln
65                  70                  75                  80


Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His Ser Glu
                85                  90                  95


Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr Asp Gln
                100                 105                 110


Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr Pro Asp
            115                 120                 125
```

Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val Phe Phe
  130   135   140

Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu Asp Tyr
145   150   155   160

Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu Glu Ala
          165   170   175

Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr Tyr Leu
      180   185   190

Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser Ser Asn
     195   200   205

Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val
  210   215   220

Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys
225   230   235   240

Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile
          245   250   255

Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile
      260   265   270

Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys
     275   280   285

Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
  290   295   300

Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr Ser Tyr
305   310   315   320

Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys
          325   330   335

Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
      340   345   350

Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu Leu Pro
      355   360   365

Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu Asp Leu
  370   375   380

```
Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr Asn Leu
385             390             395             400


Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu Glu Gly
                405             410             415


Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp Asp Phe
            420             425             430


Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro Lys Arg
            435             440             445


Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu
        450             455             460


Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp
465             470             475             480


Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys
                485             490             495


Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr
            500             505             510


Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly Gly Ser
        515             520             525


Tyr Lys Leu Thr Leu Thr Glu Ile
    530             535
```

<210>   11
<211>   3452
<212>   DNA
<213>   MURINE

<220>
<221>   misc_feature
<222>   (2973)..(2973)
<223>   n = any nucleotide

<220>
<221>   misc_feature
<222>   (3307)..(3307)
<223>   n = any nucleotide

<400>   11
```
cgccgctccg gacccaccgc ctgccgccgc gcgccgcccg ccgccgcctc ctcccccccgg      60

atcgggtgta ctgtcccaac ccgaaagtcc agttctgcgg cccggcagcg gcgagcgagc     120
```

```
gcgatgacac aggagtacga caacaaaagg cccgtgctgg tacttcagaa tgaagccctc    180

tacccacagc ggcgctccta taccagtgag gatgaagcct ggaagtcgtt cctggaaaac    240

cctctcactg cggcaaccaa agcgatgatg agcatcaacg gagacgaaga cagcgcggct    300

gcgctgggcc tgctctatga ctactacaag gtccccagag agcgccggtc atcagccgta    360

aagcccgagg gagagcaccc agagccagag cacagcaaaa gaaacagcat accaaatgtg    420

acggagcagc ccctcatttc tgctggagaa aacagggtac aagtgctgaa aaacgtgccc    480

ttcaacatcg tcctccccca tagcaaccag ctgggcattg ataagagagg ccatctgaca    540

gctcccgata caacagtcac tgtctccata gcgaccatgc ctacccactc catcaagaca    600

gaaatccagc cgcacggctt tgctgtggga atccctccag ccgtgtacca ctctgagccc    660

accgaacgcg tggtggtttt tgaccggagc ctcagcactg atcagttcag ctctggcact    720

cagccccca atgctcagcg gaggactcca gactccacct tctccgagac cttcaaggag    780

ggcgttcagg aggttttctt cccctcggaa ctcagccttc ggatgccggg catgaattca    840

gaggactatg tctttgacaa tgtttctggg aacaactttg agtataccct ggaagcctcc    900

aagtcactgc ggcagaagca aggggacagc actatgacat acctgaataa aggccagttc    960

tatcctgtca ccttaaagga aggaagcagc aatgaaggga ttcaccaccc tatcagcaaa   1020

gttcgaagtg tgatcatggt ggtttttgct gaagacaaaa gcagagaaga ccagctgaga   1080

cactggaagt actggcactc ccgtcagcac acggccaaac agaggtgcat tgacattgct   1140

gactacaaag aaagtttcaa cactatcagc aacattgagg agatagctta taacgccatt   1200

tccttcacgt gggacatcaa tgatgaggca aaggtcttca tctctgtgaa ctgcttgagc   1260

acagatttct cttctcagaa gggtgtgaag ggcttgccac tcaacattca aatcgacaca   1320

tacagctata caaccgcag caacaagccg gttcaccggg cctactgcca gataaaggtc   1380

ttctgcgaca agggagctga aaggaaaatt cgggatgaag aacgaaaaca gagcaagaga   1440

aaagtgtctg acgttaaagt gcagctgctt ccctcacaca aacggacaga catcacagtg   1500

ttcaagccct cctggacct cgacactcag cctgtcctct tcattccgga cgtgcatttt   1560

accaacctgc agcggggcag tcatgttctt tccctcccct ctgaagaact ggaaggtgaa   1620

ggctctgtct tgaaaagagg gccattcgga accgaagatg actttggagt cctcctcct   1680

gctaagctga ctcggacaga agaacccaag agagtgctgc tctatgtccg aaaggaatca   1740

gaagaagtct tcgacgccct gatgctcaag acgccgtctt tgaagggcct gatggaggca   1800

atttcagaca agtatgatgt cccccatgac aagattggga aaatatttaa gaagtgcaaa   1860

aaagggatcc tcgtgaacat ggacgacaac attgtgaagc actactccaa tgaggacacc   1920

ttccagctgc agatagagga agccggcggc tcgtacaagc tcaccctgac agagatttaa   1980

aggggcaggg gtgggggggcg ctcggctccc aggcgtggga attcagtgaa agtgttccag   2040
```

```
ctgagaagcc caggcaccta ccctgcagaa ccttaaatat cagggaagga acctttcacg   2100

taggaaatgg cgctgtgtat accgtgctgt gttgatgttt tcttttggat agaaatccat   2160

gtgttgtttt gttgttgttg tttgaatttc tgatgtgctt agaaagcgaa gcatgagaac   2220

tttgtaccgg atctaagaga ccatgggacc gtttgggtta cctgctccac tacctgtcaa   2280

agtctgcctg tgtccataag agtggtgggc tactggctgg cgagagaggg gaaggcagta   2340

gcttgtcttt gaggcttttg tgttctcgcc tgacctcagt ctaactctga ctgccttgag   2400

gagtgggccc agccctcagc aataaagggc taagccttct ccctccacct ctcctccagt   2460

gtttactaaa tagggtgcat tcctggaacc ttttcccgca acttcccttg gacatgtgga   2520

ctgcctttct gatgaagaac ttgcgtgagt gacagtgtga agttagctct gttaaagctg   2580

cgttgtatat aagtgcaata tcttttttgaa ggtctgcctg taaatgtgta catatatgtc   2640

tgatataaat atataatata taaatgcggt gtctgtgtac agatagtgaa ggcgagcagg   2700

aagatctacc ttgaaatccc tcttagagaa gaggttaagt tattattgat aatgtggacc   2760

aagcaggtag aacgctgttt tcccaaaaac aagcaagtgt tccctagcat agcaaaaagc   2820

catctcatgt ggcagagcca tctgctcttg cgaatgttgt caccgtgtgg gtttctgcac   2880

cctgagtgga ctaatggaa gactggactg cagctactat atgaggtgtg tgtgcaggtg   2940

tcagccaagc tgtgcccatg cagagactca gcngtgtcat gagccagcga ttcaaaccaa   3000

aatgggccga ttctacaagg ccatgtttca gagcttccaa gcatcagcta ccgtgtgttt   3060

gaactggaag gcattcatga atttacataa ctgtggcagg ggaatgtttt gtgcacactt   3120

aaatatttaa gaacaaaacg aaactttaca atgtaaytttt ataatgaatc ctgtaacaga   3180

aatacaattg cgggtttctt taggttcagg gaactagaat aggtcatttg tatgagtagg   3240

attgttagcg gtatacgtar gttaaaaagt actctaatga agtatgtgaa caaaatagct   3300

ggttttntaa gatacgggat acgggtcata taacaatatt ttctattttg ttttatgaaa   3360

tcagctttac ttgtttttaat tgtatcattg aacatgtgtt ttaaaccaaa gggattgaat   3420

tttatatgtc tatttcaaaa aaaaaaaaaa aa                                 3452
```

<210> 12
<211> 618
<212> PRT
<213> MURINE

<400> 12

```
Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn
1               5                   10                  15


Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
                20                  25                  30
```

Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
        35   40   45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
        50   55   60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Ala Val Lys
65   70   75   80

Pro Glu Gly Glu His Pro Glu Pro Glu His Ser Lys Arg Asn Ser Ile
                85   90   95

Pro Asn Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
            100   105   110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn
        115   120   125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr
    130   135   140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145   150   155   160

Ile Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
                165   170   175

Ser Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr
            180   185   190

Asp Gln Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr
        195   200   205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
    210   215   220

Phe Phe Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
225   230   235   240

Asp Tyr Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
            245   250   255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr
        260   265   270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser

Ser Asn Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
    290   295   300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305   310   315   320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
            325   330   335

Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
        340   345   350

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
        355   360   365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
    370   375   380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr
385   390   395   400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
            405   410   415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
        420   425   430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu
    435   440   445

Leu Pro Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu
    450   455   460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr
465   470   475   480

Asn Leu Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu
            485   490   495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp
            500   505   510

Asp Phe Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro
            515   520   525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
    530   535   540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
545   550   555   560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
                565   .   570   575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
            580   585   590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
        595   600   605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
    610   615

<210>   13
<211>   2195
<212>   DNA
<213>   murine

<400>   13
cgcccgggca ggtcagactt gaaagtccag tttcaccaga ggctgaggct ccaggaaaag   60

gggagcgagt tcattggatc aaacatgtca caagagtcgg acaataataa aagactagtg   120

gccttagtgc ccatgcccag tgaccctccc ttcaacaccc gaagagccta cacaagtgag   180

gatgaggcct ggaagtcata tctggagaac cccctgactg cggccaccaa ggcgatgatg   240

agcatcaacg gggacgagga cagtgctgcc gccctgggcc tgctctatga ctactacaag   300

gttcctcgag acaagagact tctgtctgtg agcaaagcaa gtgacagcca agaagaccag   360

gataaaagaa actgccttgg caccagtgaa gcccagatca atttgagcgg aggcgagaac   420

agagtgcagg ttctgaagac tgtcccggtg aacctctgtc taagtcaaga ccacatggag   480

aattcgaagc gcgagcagta cagtgtatcc atcaccgaga gctctgccgt catccccgtg   540

tcaggcatca ccgtggtgaa agccgaggat ttcacaccgg tgttcatggc gccccgggtg   600

cactatcccc gcgcggacag tgaggagcag cgcgtggtta tctttgaaca gactcagtac   660

gacctgccct ccatagccag ccacagctcc tatctcaagg acgaccagcg cagcacgccg   720

gacagcacct acagcgagag ctttaaggac ggcgcctcgg agaaatttcg gagtacttct   780

gttggtgctg acgagtatac atatgaccag acgggaagtg gtacatttca gtacaccctg   840

gaagccacca atctctccg tcagaaacag ggggagggcc ccatgaccta cctcaacaaa   900

ggacaattct atgccataac actcagtgag actggagaca caaatgctt ccgacacccc   960

atcagcaaag tcaggagtgt ggtgatggtg gtctttagtg aagacaaaaa ccgagatgag 1020

Page 32

```
cagctgaaat actggaagta ctggcactcc cggcagcaca ctgccaagca gagggtcctt    1080

gacattgctg attacaagga gagcttcaac accatcggga acattgaaga gatcgcatac    1140

aatgctgttt ccttcacctg ggatgtgaac gaggaggcaa agatttttat caccgtgaat    1200

tgcctgagta cagatttctc ctcccaaaag ggtgtaaaag acttcccct gatgattcag     1260

atcgacacgt acagctacaa caaccgcagc aataaaccca tccacagagc atactgccag    1320

atcaaggtct tctgtgacaa gggagcagaa agaaaaatcc gggatgaaga gagaaagcag    1380

aacaggaaga aagggaaggg ccaggcctct caagcccagt gcaacaactc ctctgatggg    1440

aagatggccg ccataccgtt acagaagaag agtgacatca cgtacttcaa aaccatgccc    1500

gacctgcact cacagcctgt gctcttcata ccagatgttc actttgcaaa cctacagagg    1560

accggacagg tttattacaa cacagacgat gagcgagaag cagcagcgt ccttgttaag     1620

cggatgttca ggcccatgga agaggagttt ggtccaacac cgtctaagca gatcaaagaa    1680

gaaaacgtaa aacgagtgct tttatatgtg aggaaggaga acgatgacgt cttcgatgct    1740

ctgatgctga aatcacccac ggtgaagggt ctgatggaag cgctgtctga gaagtatggg    1800

ctgccagtgg agaaaatcac aaagctttat aagaagagca aaaagggcat cctggtcaac    1860

atggatgaca acatcattga gcactattca aatgaggaca ccttcatcct caacatggag    1920

agcatggtgg aaggcttcaa gatcacgctg atggagatct gagccctggg tgtcccctcg    1980

ataggagctt ttggtatact ccttcctggg agagatggga tctctgccgc cccaggacct    2040

ggagacccac ccatctcact cacctctcaa gactgttaca agactgctgg gaagggggc     2100

agggcccaag gcccagtaat ggacttcctt caactcttcc acttgctccc tatggagctg    2160

aagcctgagc ccctcagcaa atttcttctc gtgcc                               2195
```

<210> 14
<211> 625
<212> PRT
<213> murine

<400> 14

```
Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1               5                   10                  15


Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
            20                  25                  30


Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
        35                  40                  45


Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
    50                  55                  60
```

```
Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65              70              75                      80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Asp Lys Arg Asn
                85              90                  95

Cys Leu Gly Thr Ser Glu Ala Gln Ile Asn Leu Ser Gly Gly Glu Asn
            100             105             110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Cys Leu Ser Gln
        115             120             125

Asp His Met Glu Asn Ser Lys Arg Glu Gln Tyr Ser Val Ser Ile Thr
    130             135             140

Glu Ser Ser Ala Val Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145             150             155             160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
            165             170             175

Ala Asp Ser Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
            180             185             190

Asp Leu Pro Ser Ile Ala Ser His Ser Ser Tyr Leu Lys Asp Asp Gln
        195             200             205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Gly Ala
    210             215             220

Ser Glu Lys Phe Arg Ser Thr Ser Val Gly Ala Asp Glu Tyr Thr Tyr
225             230             235             240

Asp Gln Thr Gly Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
            245             250             255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
            260             265             270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
        275             280             285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
    290             295             300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
```

Page 34

305   310   315   320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
                325   330   335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
                340   345   350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
                355   360   365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
        370   375   380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385   390   395   400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
                405   410   415

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
                420   425   430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Ala Gln Cys Asn Asn
                435   440   445

Ser Ser Asp Gly Lys Met Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
        450   455   460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465   470   475   480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
                485   490   495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Ser Ser Val Leu Val Lys
                500   505   510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Thr Pro Ser Lys
                515   520   525

Gln Ile Lys Glu Glu Asn Val Lys Arg Val Leu Leu Tyr Val Arg Lys
        530   535   540

Glu Asn Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545   550   555   560

```
Lys Gly Leu Met Glu Ala Leu Ser Glu Lys Tyr Gly Leu Pro Val Glu
            565             570                 575


Lys Ile Thr Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
            580             585                 590


Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
            595             600                 605


Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Ile Thr Leu Met Glu
            610             615                 620


Ile
625
```

```
<210>   15
<211>   2831
<212>   DNA
<213>   murine

<220>
<221>   CDS
<222>   (200)..(2008)


<220>
<221>   misc_feature
<222>   (2806)..(2806)
<223>   n = any nucleotide


<400>   15
acctgtgctt ccagccaatc agcgccaccg cagccgggga ccgctgtcag caaaatctca      60

acatccagag cgcaacgtag agcaaacgct tccccgggca ggaagggaat gtctgtgtca     120

gaggagaatt aagagacgag tggtcagcag cgcctgcgag ccaaccagag acggatcgct     180

ggaacctcgg agaaggaag atg tcg aat gaa ctt gat ttc agg tct gtg cgg     232
                     Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg
                      1               5                   10

ttg ctg aag aat gac cct gtg agc ttc cag aag ttt ccc tac agt aat     280
Leu Leu Lys Asn Asp Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn
            15                  20                  25

gag gac gag gcc tgg aag aca tac ctg gag aac cct ttg acg gct gcc     328
Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
            30                  35                  40

acc aaa gcc atg atg aga gtc aac ggg gac gag gag agt gtg gct gct     376
Thr Lys Ala Met Met Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala
            45                  50                  55

ctg agc ttc ctc tac gac tac tat atg ggt ccc aag gag aag cgg ata     424
Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
60                  65                  70                  75
```

```
ctg tcc tcc agc act ggt ggc cgg aat gac caa gga aag aag ttc tac    472
Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr
            80              85                  90

cac agc atg gac tat gag ccg gat ctt gcc ccc ctc gag agc ccc aca    520
His Ser Met Asp Tyr Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr
            95              100                 105

cac ctc atg aaa ttt ttg aca gag aac gtg tct gga agt cca gac tac    568
His Leu Met Lys Phe Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr
            110             115                 120

aca gac cag ctc aag aaa aac aat ctg cta ggc ttg gag ggg gtt cta    616
Thr Asp Gln Leu Lys Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu
            125             130                 135

ccc acc ccc ggc aag acc aat acc gtc ccc cca ggt ccg agt aaa ctg    664
Pro Thr Pro Gly Lys Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu
140             145                 150                 155

gaa gcc agc tcc atg gac agc tac ctc ttg ccc gcc agt gac ata tat    712
Glu Ala Ser Ser Met Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr
            160             165                 170

gac aat ggc tcc ctc aac tca tta ttt gag agc att cat ggg gtt cca    760
Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
            175             180                 185

ccc aca cag cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag    808
Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
            190             195                 200

gag tct ctg ctc ttc cct gat att ctg aag aca tcc ccg gac ccc cca    856
Glu Ser Leu Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro
            205             210                 215

tgc cca gag gat tat cca ggc ctc aag agt gac ttt gaa tac acc ctg    904
Cys Pro Glu Asp Tyr Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu
220             225                 230                 235

ggc tcc ccc aaa gcc att cac atc aaa gca ggg gag tca ccc atg gcc    952
Gly Ser Pro Lys Ala Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala
            240             245                 250

tac ctc aac aag ggt cag ttc tac ccc gtc acc cta cgc acc cca gca   1000
Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
            255             260                 265

gga ggg aaa ggc ctc gct ctg tcc tcc agc aaa gtc aag agc gtg gtg   1048
Gly Gly Lys Gly Leu Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val
            270             275                 280

atg gtc gtg ttc gat aat gac aag gtc ccc gtg gag cag ctg cgt ttc   1096
Met Val Val Phe Asp Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe
            285             290                 295

tgg agg cac tgg cat tcc cgg cag ccc acc gcc aag cag cgc gtc atc   1144
Trp Arg His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile
300             305                 310                 315

gac gta gct gac tgt aag gaa aac ttc aac acg gtc cag cac att gaa   1192
Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu
            320             325                 330
```

```
gag gtg gcc tat aac gcg ctg tcc ttt gtg tgg aat gtc aac gag gaa    1240
Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu
        335             340             345

gcc aag gtg ttt atc ggt gtc aac tgt ctg agc aca gac ttc tcc tcg    1288
Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
        350             355             360

cag aag gga gtg aag ggt gtc ccc ctg aac ttg caa att gac acc tat    1336
Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
        365             370             375

gac tgt gga gca ggc act gag cgc ctg gta cac cgt gct gtc tgc cag    1384
Asp Cys Gly Ala Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln
380             385             390             395

atc aag atc ttc tgt gat aag gga gct gag agg aag atg cgc gat gat    1432
Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp
                400             405             410

gaa cgg aag cag ttt cga agg aag gtc aag tgc cca gac tcc agt aac    1480
Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn
        415             420             425

aat gca gga atc aag ggc tgc ctg ctg tca ggc ttc agg ggc aat gag    1528
Asn Ala Gly Ile Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu
        430             435             440

acc aca tac ttg cgg cca gaa act gac ctg gag acc cag cct gtg ttg    1576
Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu
        445             450             455

ttt atc ccc aat ctg cat ttt tcc agc cta cag cgc cca gga ggg gtt    1624
Phe Ile Pro Asn Leu His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val
460             465             470             475

gtc ccc tca gca gga cac agc agc tct gac agg ctg cct ctg aag cga    1672
Val Pro Ser Ala Gly His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg
                480             485             490

acc tgc tca ccc ttt gct gag gag ttt gag cct ctt cct tct aaa caa    1720
Thr Cys Ser Pro Phe Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln
                495             500             505

gcc aag gaa gat gac ctt cag aga gtt ctg ttg tat gtg agg agg gag    1768
Ala Lys Glu Asp Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu
        510             515             520

aca gag gag gtg ttt gac gcg ctc atg ttg aag acc ccg gac ctg aag    1816
Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys
        525             530             535

ggc ctg agg aat gcg atc tct gag aag tac ggc ctc ccc gag gag aat    1864
Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn
540             545             550             555

att tgc aaa gtc tac aag aaa tgc aag cga ggc atc ctg gtt aac atg    1912
Ile Cys Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met
                560             565             570

gac aac aac atc atc caa cac tac agc aac cac gtg gcc ttc ctg ctg    1960
Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu
```

575   580   585

```
gac atg ggt gag ctg gac ggc aag atc cag atc atc ctg aag gag cta     2008
Asp Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
        590                     595                     600

tgagggcccg gcctcaagcg tcccacaccc ggggcccggc tcaagccacg tacaacctct     2068

tctgtgtcag ctgttacttg aaatgccttt ctttgggaaa gaggtctcgc aagcaaccaa     2128

ctcggtgatg tccaagccag ggagagacca agaaggttcc aggatctaaa tgtcccaccc     2188

aggctcgaac tcactccaga gcttcctgaa agcacccagc ccaccggaga gtctgagcaa     2248

cacagaccca actgcctgct ttctcttcta agtcccgctg cagaggccct tacaggggac     2308

gggggtcaca ccaccttctc tgcagggcta cacccgctgt ctcgatcggt tctgacgttc     2368

actgtttcct ttctaccaac ttcagaccag agagttctca cactttggcc aaataacttg     2428

aaaactcgtg actttcacag cagatgcctt tgtgaggccc ttggagagga aactttctta     2488

ttgacttcct cggcacaaga tgtaagtcac catcatcgag ctgacaggaa caaataccct     2548

tgccacctac tgttgtacac atttcttatt tacagttttc attatgtgat tatatatata     2608

tatatgtaag tatatattat gtacatatat gcaacatttt gtatgtccat gttacatttt     2668

tatcatttca aaaatatgta tttcatattt cttgaactat tttttagct gttattcgat      2728

tatgcatttt gtatatcata gggtttagta ataaaagcct acccatgcac acttaaaaaa     2788

aaaaaaaaaa aaatatcnag cttatcgata ccgtcgacct cga                       2831
```

<210> 16
<211> 603
<212> PRT
<213> murine

<400> 16

```
Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg Leu Leu Lys Asn Asp
1               5                  10                  15


Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn Glu Asp Glu Ala Trp
            20                  25                  30


Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met
        35                  40                  45


Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr
    50                  55                  60


Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser Ser Thr
65                  70                  75                  80
```

Page 39

```
Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr His Ser Met Asp Tyr
            85              90              95

Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr His Leu Met Lys Phe
            100             105             110

Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr Thr Asp Gln Leu Lys
            115             120             125

Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu Pro Thr Pro Gly Lys
    130             135             140

Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu Glu Ala Ser Ser Met
145             150             155             160

Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr Asp Asn Gly Ser Leu
            165             170             175

Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln Arg Trp
            180             185             190

Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Leu Leu Phe
            195             200             205

Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro Cys Pro Glu Asp Tyr
            210             215             220

Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro Lys Ala
225             230             235             240

Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala Tyr Leu Asn Lys Gly
            245             250             255

Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys Gly Leu
            260             265             270

Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val Met Val Val Phe Asp
            275             280             285

Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe Trp Arg His Trp His
    290             295             300

Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala Asp Cys
305             310             315             320

Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu Glu Val Ala Tyr Asn
            325             330             335
```

Page 40

Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val Phe Ile
340   345   350

Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val Lys
        355   360   365

Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly Ala Gly
    370   375   380

Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile Phe Cys
385   390   395   400

Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys Gln Phe
            405   410   415

Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Asn Ala Gly Ile Lys
            420   425   430

Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu Arg
        435   440   445

Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu Phe Ile Pro Asn Leu
    450   455   460

His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val Val Pro Ser Ala Gly
465   470   475   480

His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe
            485   490   495

Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Asp Asp
            500   505   510

Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe
        515   520   525

Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala
    530   535   540

Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn Ile Cys Lys Val Tyr
545   550   555   560

Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile Ile
            565   570   575

Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu Leu
    580   585   590

Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
        595   600

```
<210>   17
<211>   4840
<212>   DNA
<213>   drosphila

<400>   17
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc     60

cgaaccgacc cgccccctca acttttgcgc cctccagtag caatagcagc aatatgagca    120

gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa    180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa    240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc    300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc    360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca    420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc    480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag    540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca    600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa    660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag    720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg    780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat    840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg    900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag    960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc   1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc   1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg   1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa   1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac   1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg   1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc   1380

aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag   1440

atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa   1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt   1560
```

```
gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca   1620

gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca atgatcacgg gcaggcggta   1680

tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat   1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca   1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg   1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa   1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact   1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac   2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag   2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt   2160

ggaaagctca atggccagac cacacctatc gatgtctctg gcctatcgca aaatgagatt   2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt   2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag   2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc   2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag   2460

caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac   2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca tacccaaaa gtcctttgat   2580

tatacggaat tgtgccagcc gggcacgctg atcgatgcca atggcagcat acccgtcagc   2640

gtgaacagca tccagcagag aacggcggtc catggcagcc agaacagtcc caccacatcg   2700

ctggtggaca ccagcaccaa tggatccacg cgatcgcggc cctggcacga ctttggacgt   2760

cagaatgatg ccgacaaaat acaaatacca aaaatcttca caaacgtggg cttccgatat   2820

cacctggaga gccccatcag ttcatcgcag aggcgcgagg acgatcgcat cacctacatc   2880

aacaagggtc aattctatgg aataacgctg gagtatgtgc acgatgcgga aaagcccatt   2940

aagaacacca ccgtcaagag tgtgatcatg ctaatgttcc gcgaggagaa gagtcccgag   3000

gatgagatca aggcctggca`attctggcac agtcgtcagc attccgtgaa gcagagaatc   3060

ttggatgcag atacgaagaa ctcggttggc ctcgttggct gcatcgagga agtgtcgcac   3120

aatgccatcg ccgtctactg gaatccgctg gagagctccg ccaagatcaa cattgcggtt   3180

cagtgcttga gcacggattt cagcagtcaa aagggaggcc tgccgctgca cgtacaaatc   3240

gacacatttg aggaccccag agatacggcg gtcttccacc gcggctactg tcagataaag   3300

gtcttctgcg ataagggcgc cgaacgaaag acgcgcgatg aagagcggcg ggccgccaaa   3360

cgaaagatga cagccacggg cagaaagaag ctggacgagc tttaccatcc ggtaacggat   3420
```

Page 43

```
cggtccgagt tctatggcat gcaggacttc gccaagccgc cggtgctatt ctcgcccgcc   3480

gaggacatgg agaaggtagg tcagctgggc attggcgctg ccaccggcat gacattcaac   3540

cccctgagca acggcaactc caactccaac tcgcactcgt ccttgcagag cttctacggc   3600

catgagactg actcgccgga cctgaagggg gcctcaccgt tcctgctcca cggccagaag   3660

gtggccacgc cgacgctcaa gttccacaac cattttccgc ccgacatgca gaccgataag   3720

aaggatcaca tactggacca gaacatgttg accagcacac ccctgaccga ctttggtccg   3780

ccgatgaagc gcggcaggat gacgccgccg acctcggaac gcgtgatgct gtacgtgcgg   3840

caggagaacg aggaggtgta tacaccgttg cacgtggtgc cgcccaccac gatcggcctg   3900

ctaaatgcga ttgaaaacaa atacaaaatc tcaacaacga gcataaataa catttatcgc   3960

acaaacaaga aggggattac tgcgaaaatt gacgatgaca tgatatcgtt ctactgcaac   4020

gaggacatct ttctgctgga ggtgcaacag atcgaggacg acctgtacga tgtgacgctc   4080

acggagctgc ccaatcagta gcgctggcag tacgggtagc acccgctaac cgcactcaaa   4140

aaaaaaagca aacaaacaca caaattacgg acacaacaag ttgtttcaat aagccatttt   4200

ccatagagcc taagtctaaa tatcgtagtt ataataatgg gatccgcaac aaatcgagtt   4260

gcaacgaatg ttaagaacgc taacacaata cgcatgtaaa atgatacttt aaaattgatt   4320

tagttatttt agcaacaatg agattatcta aaattgtttg atcaaatttt acattctcgc   4380

tatgtctata gataattcta agcccgtaag cccataagcg taatcgtaat cgtaatcgta   4440

ccgtgtattt atgctcatat ataaacaact atatatatat atatatatat atatatgtgc   4500

ggagtgcaac agtgtctgtc cagtaggaga taagtctcgt ttccgctccc ctgcttatgc   4560

tatgacctta ggtccagggc aagtatgagt taccgaatct atctattagg tgcatctaac   4620

gaaaggaatc attagctctg cacgaactct agccgtagcc tattgtaatc catttgtatg   4680

tttggcttaa gcgttttact tgttgaatat aaagtgtaaa attatttttg aaaaaaaaaa   4740

acccacacaa aacacaaatc gtttgttcta tatttctgtt tcaaaactaa ctcgttaccc   4800

acaatcccct ctgttatgta taattaggat ctctgtacac                         4840
```

<210> 18
<211> 1061
<212> PRT
<213> murine

<400> 18

```
Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1               5                   10                  15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20                  25                  30
```

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
         35   40   45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50   55   60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65   70   75   80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
            85   90   95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
            100   105   110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115   120   125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
            165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
            180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
        195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
    210   215   220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
            245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
        260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
    275   280   285

Page 45

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
            325   330   335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
          340   345   350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
    355   360   365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
370   375   380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385   390   395   400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
          405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
          420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
         435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
    450   455   460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
          485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
          500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
        515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly

                    530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
545   550   555   560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
                565   570   575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
            580   585   590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
        595   600   605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
    610   615   620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625   630   635   640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
                645   650   655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
                660   665   670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
            675   680   685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
    690   695   700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705   710   715   720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
                725   730   735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
                740   745   750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
        755   760   765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
    770   775   780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785   790   795   800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
                805   810   815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
            820   825   830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
            835   840   845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Val Gly Gln Leu
    850   855   860

Gly Ile Gly Ala Ala Thr Gly Met Thr Phe Asn Pro Leu Ser Asn Gly
865   870   875   880

Asn Ser Asn Ser Asn Ser His Ser Ser Leu Gln Ser Phe Tyr Gly His
            885   890   895

Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu His
            900   905   910

Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe Pro
        915   920   925

Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met
    930   935   940

Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly
945   950   955   960

Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln
            965   970   975

Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr
            980   985   990

Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
        995   1000   1005

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
    1010   1015   1020

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
    1025   1030   1035

```
Phe Leu  Leu Glu Val Gln Gln  Ile Glu Asp Asp Leu  Tyr Asp Val
    1040                  1045              1050

Thr Leu  Thr Glu Leu Pro Asn  Gln
    1055              1060
```

<210> 19
<211> 21
<212> DNA
<213> human

<400> 19
gaagtctttg atgccctgat g   21

<210> 20
<211> 21
<212> DNA
<213> human

<220>
<221> misc_feature
<223> human p49 mgr

<400> 20
aacccattcc ctcgacatag a   21

<210> 21
<211> 20
<212> DNA
<213> human

<400> 21
agcgcgatga cacaggagta   20

<210> 22
<211> 20
<212> DNA
<213> human

<400> 22
cgttgctatg gagacagtga   20

<210> 23
<211> 20
<212> DNA
<213> human

<400> 23
ccgtttaaca aggacactgc   20

<210> 24
<211> 20
<212> DNA
<213> murine

<400> 24
ctggaagcca ccaaatctct   20

<210> 25
<211> 20
<212> DNA
<213> murine

<400> 25
agcgcgatga cacaggagta   20

<210> 26
<211> 20
<212> DNA
<213> murine

<400> 26
agtgccagag ctgaactgat   20

<210> 27
<211> 20
<212> DNA
<213> murine

<400> 27
tccatgggtt ccttgagttc   20

<210> 28
<211> 20
<212> DNA
<213> murine

<400> 28
agtgccagag ctgaactgat   20

<210> 29
<211> 20
<212> DNA
<213> murine

<400> 29
aaaggggagc gagttcattg   20

<210> 30
<211> 20
<212> DNA
<213> murine

<400> 30
agagctctcg gtgatggata   20

<210> 31
<211> 34
<212> DNA
<213> drosophila dopa decarboxylase promoter

<400> 31
ggtggtgctc taataaccgg tttccaagat gcgc   34

<210> 32
<211> 34
<212> DNA
<213> drosophila PCNA promoter

<400> 32
gggtaaaaag tgtgaacaat caaaccagtt ggca   34

<210> 33
<211> 84
<212> DNA
<213> human

<400> 33
ggacacacac ccaaacccac acccacccac aaacacacaa accggcagtg acaacaacca   60

cccatccttc aataacagca acca   84

<210> 34
<211> 4747
<212> DNA
<213> Drosophila

<400> 34
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc   60

cgaaccgacc cgcccccтca acttttgcgc cctccagtag caatagcagc aatatgagca   120

gcagcaacat caaatgttag gccaaaatgc acaaccgcc agcaacaaag gcagcaccaa   180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa   240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc   300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc   360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca   420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc   480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag   540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca   600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa   660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag   720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg   780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat   840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg   900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag   960

```
ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc    1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc    1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg    1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa    1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac    1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg    1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc    1380

aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag    1440

atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa    1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt    1560

gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca    1620

gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca atgatcacgg gcaggcggta    1680

tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat    1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca    1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg    1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa    1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact    1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac    2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag    2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt    2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt    2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt    2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag    2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc    2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag    2460

caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac    2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaa gtcctttgat    2580

tatacggaat tgtgccagcc gggcacgctg atcgatgcca atggcagcat acccgtcagc    2640

gtgaacagca tccagcagag aacggcggtc catggcagcc agaacagtcc caccacatcg    2700

ctggtggaca ccagcaccaa tggatccacg cgatcgcggc cctggcacga ctttggacgt    2760

cagaatgatg ccgacaaaat acaaatacca aaaatcttca caaacgtggg cttccgatat    2820

cacctggaga gccccatcag ttcatcgcag aggcgcgagg acgatcgcat cacctacatc    2880
```

Page 52

```
aacaagggtc aattctatgg aataacgctg gagtatgtgc acgatgcgga aaagcccatt   2940

aagaacacca ccgtcaagag tgtgatcatg ctaatgttcc gcgaggagaa gagtcccgag   3000

gatgagatca aggcctggca attctggcac agtcgtcagc attccgtgaa gcagagaatc   3060

ttggatgcag atacgaagaa ctcggttggc ctcgttggct gcatcgagga agtgtcgcac   3120

aatgccatcg ccgtctactg gaatccgctg gagagctccg ccaagatcaa cattgcggtt   3180

cagtgcttga gcacggattt cagcagtcaa aagggaggcc tgccgctgca cgtacaaatc   3240

gacacatttg aggaccccag agatacggcg gtcttccacc gcggctactg tcagataaag   3300

gtcttctgcg ataagggcgc cgaacgaaag acgcgcgatg aagagcggcg ggccgccaaa   3360

cgaaagatga cagccacggg cagaaagaag ctggacgagc tttaccatcc ggtaacggat   3420

cggtccgagt tctatggcat gcaggacttc gccaagccgc cggtgctatt ctcgcccgcc   3480

gaggacatgg agaagagctt ctacggccat gagactgact cgccggacct gaaggggggcc   3540

tcaccgttcc tgctccacgg ccagaaggtg gccacgccga cgctcaagtt ccacaaccat   3600

tttccgcccg acatgcagac cgataagaag gatcacatac tggaccagaa catgttgacc   3660

agcacacccc tgaccgactt tggtccgccg atgaagcgcg gcaggatgac gccgccgacc   3720

tcggaacgcg tgatgctgta cgtgcggcag gagaacgagg aggtgtatac accgttgcac   3780

gtggtgccgc ccaccacgat cggcctgcta aatgcgattg aaaacaaata caaaatctca   3840

acaacgagca taaataacat ttatcgcaca aacaagaagg ggattactgc gaaaattgac   3900

gatgacatga tatcgttcta ctgcaacgag gacatctttc tgctggaggt gcaacagatc   3960

gaggacgacc tgtacgatgt gacgctcacg gagctgccca atcagtagcg ctggcagtac   4020

gggtagcacc cgctaaccgc actcaaaaaa aaaagcaaac aaacacacaa attacggaca   4080

caacaagttg tttcaataag ccattttcca tagagcctaa gtctaaatat cgtagttata   4140

ataatgggat ccgcaacaaa tcgagttgca acgaatgtta agaacgctaa cacaatacgc   4200

atgtaaaatg atactttaaa attgatttag ttattttagc aacaatgaga ttatctaaaa   4260

ttgtttgatc aaattttaca ttctcgctat gtctatagat aattctaagc ccgtaagccc   4320

ataagcgtaa tcgtaatcgt aatcgtaccg tgtatttatg ctcatatata aacaactata   4380

tatatatata tatatatata tatgtgcgga gtgcaacagt gtctgtccag taggagataa   4440

gtctcgtttc cgctcccctg cttatgctat gaccttaggt ccagggcaag tatgagttac   4500

cgaatctatc tattaggtgc atctaacgaa aggaatcatt agctctgcac gaactctagc   4560

cgtagcctat tgtaatccat ttgtatgttt ggcttaagcg ttttacttgt tgaatataaa   4620

gtgtaaaatt atttttgaaa aaaaaaaacc cacacaaaac acaaatcgtt tgttctatat   4680

ttctgtttca aaactaactc gttacccaca atcccctctg ttatgtataa ttaggatctc   4740
```

Page 53

<210>   35
<211>   1030
<212>   PRT
<213>   Drosophila

<400>   35

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1   5   10   15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20   25   30

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
        35   40   45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50   55   60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65   70   75   80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
                85   90   95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
                100   105   110 .

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
            115   120   125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
                165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
                180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
            195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
                245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
            260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
        275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
                325   330   335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
                340   345   350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
        355   360   365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
    370   375   380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385   390   395   400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
            405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
            420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
        435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
    450   455   460

Page 55

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
        485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
        500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
        515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
    530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
545   550   555   560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
        565   570   575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
        580   585   590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
        595   600   605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
    610   615   620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625   630   635   640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
            645   650   655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
        660   665   670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
        675   680   685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
    690   695   700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705   710   715   720

Page 56

```
Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
                725             730             735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
                740             745             750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
                755             760             765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
        770             775             780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785             790             795             800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
                805             810             815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
                820             825             830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
            835             840             845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Ser Phe Tyr Gly
    850             855             860

His Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu
865             870             875             880

His Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe
                885             890             895

Pro Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn
            900             905             910

Met Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg
        915             920             925

Gly Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg
    930             935             940

Gln Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr
945             950             955             960

Thr Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr
                965             970             975
```

Page 57

Thr Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
        980   985   990

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile Phe
        995   1000   1005

Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val Thr
        1010   1015   1020

Leu Thr Glu Leu Pro Asn Gln
        1025   1030


```
<210>   36
<211>   5650
<212>   DNA
<213>   Drosophila

<400>   36
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc    60

cgaaccgacc cgcccccctca acttttgcgc cctccagtag caatagcagc aatatgagca   120

gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa   180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa   240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc   300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc   360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca   420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc   480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag   540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca   600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa   660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag   720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg   780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat   840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg   900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag   960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc  1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc  1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg  1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa  1200
```

```
ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac   1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg   1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc   1380

aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag   1440

atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa   1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt   1560

gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca   1620

gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca tgatcacgg gcaggcggta   1680

tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat   1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca   1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg   1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa   1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact   1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac   2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag   2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt   2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt   2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt   2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag   2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc   2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag   2460

caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac   2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaaa gatcttgcac   2580

gtggatgcac caacggcaag tgaagctgat aggcccagca cacccagcag cagcatcaac   2640

agcactgaaa acactgaatc ggactcacag tcagtatcag gatcagaatc aggatcgccg   2700

ggagccagga ccacagccac actagagatg tatgcaacca cgggcggcac acagatctat   2760

ctacagacct cacatcccag cacggcgagc ggagcgggcg gcggcgccgg acccgctgga   2820

gccgccggcg gcggcggtgt gtccatgcag gcgcaaagtc ccagtccggg tccctatatc   2880

acggccaatg actatggcat gtacacggcc agtcgcctgc cacccggtcc cccgcccacc   2940

agcaccacca cgtttatagc ggagccctcc tactatcggg aatactttgc accggatggc   3000

caaggtggct atgtgccggc cagcacgagg tctttgtatg cgacgtgga cgtatccgta   3060
```

tctcagcccg gcggagtggt cacctatgag ggccgctttg ccggcagcgt tcccccgccc   3120

gccaccacca ccgtgctaac cagcgtgcat caccaccagc aacagcagca gcaacaacag   3180

cagcatcaac agcagcagca gcagcaacag caccaccagc agcaacagca ccattcgcag   3240

gatggcaaga gcaatggcgg agcaacgcca ctctatgcca aagccattac ggcggcgggt   3300

ctaacggtgg atttgccaag tccggattcg ggcattggta cggatgccat tacaccgcgg   3360

gatcagacaa atatccaaca gtcctttgat tatacggaat tgtgccagcc gggcacgctg   3420

atcgatgcca atggcagcat acccgtcagc gtgaacagca tccagcagag aacggcggtc   3480

catggcagcc agaacagtcc caccacatcg ctggtggaca ccagcaccaa tggatccacg   3540

cgatcgcggc cctggcacga ctttggacgt cagaatgatg ccgacaaaat acaaatacca   3600

aaaatcttca caaacgtggg cttccgatat cacctggaga gccccatcag ttcatcgcag   3660

aggcgcgagg acgatcgcat cacctacatc aacaagggtc aattctatgg aataacgctg   3720

gagtatgtgc acgatgcgga aaagcccatt aagaacacca ccgtcaagag tgtgatcatg   3780

ctaatgttcc gcgaggagaa gagtcccgag gatgagatca aggcctggca attctggcac   3840

agtcgtcagc attccgtgaa gcagagaatc ttggatgcag atacgaagaa ctcggttggc   3900

ctcgttggct gcatcgagga agtgtcgcac aatgccatcg ccgtctactg gaatccgctg   3960

gagagctccg ccaagatcaa cattgcggtt cagtgcttga cacggattt cagcagtcaa   4020

aagggaggcc tgccgctgca cgtacaaatc gacacatttg aggaccccag agatacggcg   4080

gtcttccacc gcggctactg tcagataaag gtcttctgcg ataagggcgc cgaacgaaag   4140

acgcgcgatg aagagcggcg ggccgccaaa cgaaagatga cagccacggg cagaaagaag   4200

ctggacgagc tttaccatcc ggtaacggat cggtccgagt tctatggcat gcaggacttc   4260

gccaagccgc cggtgctatt ctcgcccgcc gaggacatgg agaaggtagg tcagctgggc   4320

attggcgctg ccaccggcat gacattcaac cccctgagca acggcaactc caactccaac   4380

tcgcactcgt ccttgcagag cttctacggc catgagactg actcgccgga cctgaagggg   4440

gcctcaccgt tcctgctcca cggccagaag gtggccacgc cgacgctcaa gttccacaac   4500

cattttccgc ccgacatgca gaccgataag aaggatcaca tactggacca gaacatgttg   4560

accagcacac ccctgaccga ctttggtccg ccgatgaagc gcggcaggat gacgccgccg   4620

acctcggaac gcgtgatgct gtacgtgcgg caggagaacg aggaggtgta taccgttg   4680

cacgtggtgc cgcccaccac gatcggcctg ctaaatgcga ttgaaaacaa atacaaaatc   4740

tcaacaacga gcataaataa catttatcgc acaaacaaga aggggattac tgcgaaaatt   4800

gacgatgaca tgatatcgtt ctactgcaac gaggacatct ttctgctgga ggtgcaacag   4860

atcgaggacg acctgtacga tgtgacgctc acggagctgc ccaatcagta gcgctggcag   4920

tacgggtagc acccgctaac cgcactcaaa aaaaaagca aacaaacaca caaattacgg   4980

Page 60

```
acacaacaag ttgtttcaat aagccatttt ccatagagcc taagtctaaa tatcgtagtt    5040

ataataatgg gatccgcaac aaatcgagtt gcaacgaatg ttaagaacgc taacacaata    5100

cgcatgtaaa atgatacttt aaaattgatt tagttatttt agcaacaatg agattatcta    5160

aaattgtttg atcaattttt acattctcgc tatgtctata gataattcta agcccgtaag    5220

cccataagcg taatcgtaat cgtaatcgta ccgtgtattt atgctcatat ataaacaact    5280

atatatatat atatatatat atatatgtgc ggagtgcaac agtgtctgtc cagtaggaga    5340

taagtctcgt ttccgctccc ctgcttatgc tatgacctta ggtccagggc aagtatgagt    5400

taccgaatct atctattagg tgcatctaac gaaaggaatc attagctctg cacgaactct    5460

agccgtagcc tattgtaatc catttgtatg tttggcttaa gcgttttact tgttgaatat    5520

aaagtgtaaa attatttttg aaaaaaaaaa acccacacaa aacacaaatc gtttgttcta    5580

tatttctgtt tcaaaactaa ctcgttaccc acaatcccct ctgttatgta taattaggat    5640

ctctgtacac                                                           5650
```

```
<210>  37
<211>  1331
<212>  PRT
<213>  Drosophila

<400>  37
```

```
Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1               5                   10                  15


Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20                  25                  30


Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
        35                  40                  45


Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50                  55                  60


Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65                  70                  75                  80


Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
                85                  90                  95


Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
                100                 105                 110


Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115                 120                 125
```

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
            165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
        180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
      195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
    210   215   220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
        245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
        260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
      275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
          325   330   335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
        340   345   350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
      355   360   365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu

370   375   380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385   390   395   400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
                405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
                420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
            435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
        450   455   460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
                485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
            500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
        515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
    530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545   550   555   560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
            565   570   575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
            580   585   590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
        595   600   605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
    610   615   620

Page 63

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
625   630   635   640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
                645   650   655

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
            660   665   670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
        675   680   685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
    690   695   700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705   710   715   720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
            725   730   735

Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln Gln
            740   745   750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln His His Gln
        755   760   765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
    770   775   780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785   790   795   800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
            805   810   815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
            820   825   830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
        835   840   845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
    850   855   860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865   870   875   880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys
                  885   890   895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
              900   905   910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
          915   920   925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
    930   935   940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
945   950   955   960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
              965   970   975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
          980   985   990

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
          995   1000   1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
    1010   1015   1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
    1025   1030   1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
    1040   1045   1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
    1055   1060   1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
    1070   1075   1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
    1085   1090   1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
    1100   1105   1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
    1115   1120   1125

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
    1130   1135   1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
    1145   1150   1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
    1160   1165   1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
    1175   1180   1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
    1190   1195   1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
    1205   1210   1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr
    1220   1225   1230

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn
    1235   1240   1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile
    1250   1255   1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
    1265   1270   1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
    1280   1285   1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
    1295   1300   1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
    1310   1315   1320

Thr Leu Thr Glu Leu Pro Asn Gln
    1325   1330

<210> 38
<211> 5557
<212> DNA
<213> Drosophila

<400> 38

```
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc      60

cgaaccgacc cgccccctca acttttgcgc cctccagtag caatagcagc aatatgagca     120

gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa     180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa     240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc     300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc     360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca     420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc     480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag     540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca     600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa     660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag     720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg     780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat     840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg     900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag     960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc    1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc    1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg    1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa    1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac    1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg    1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc    1380

aaccagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag    1440

atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa    1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt    1560

gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca    1620

gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca atgatcacgg gcaggcggta    1680

tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat    1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca    1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg    1860
```

Page 67

```
aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa    1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact    1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac    2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag    2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt    2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt     2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt    2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag    2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc    2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag    2460

caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac    2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaa gatcttgcac    2580

gtggatgcac caacggcaag tgaagctgat aggcccagca cacccagcag cagcatcaac    2640

agcactgaaa acactgaatc ggactcacag tcagtatcag gatcagaatc aggatcgccg    2700

ggagccagga ccacagccac actagagatg tatgcaacca cgggcggcac acagatctat    2760

ctacagacct cacatcccag cacggcgagc ggagcgggcg gcggcgccgg acccgctgga    2820

gccgccggcg gcggcggtgt gtccatgcag gcgcaaagtc ccagtccggg tccctatatc    2880

acggccaatg actatggcat gtacacggcc agtcgcctgc cacccggtcc cccgcccacc    2940

agcaccacca cgttttatagc ggagccctcc tactatcggg aatactttgc accggatggc    3000

caaggtggct atgtgccggc cagcacgagg tctttgtatg gcgacgtgga cgtatccgta    3060

tctcagcccg gcggagtggt cacctatgag ggccgctttg ccggcagcgt tcccccgccc    3120

gccaccacca ccgtgctaac cagcgtgcat caccaccagc aacagcagca gcaacaacag    3180

cagcatcaac agcagcagca gcagcaacag caccaccagc agcaacagca ccattcgcag    3240

gatggcaaga gcaatggcgg agcaacgcca ctctatgcca aagccattac ggcggcgggt    3300

ctaacggtgg atttgccaag tccggattcg ggcattggta cggatgccat tacaccgcgg    3360

gatcagacaa atatccaaca gtcctttgat tatacggaat tgtgccagcc gggcacgctg    3420

atcgatgcca atggcagcat acccgtcagc gtgaacagca tccagcagag aacggcggtc    3480

catggcagcc agaacagtcc caccacatcg ctggtggaca ccagcaccaa tggatccacg    3540

cgatcgcggc cctggcacga ctttggacgt cagaatgatg ccgacaaaat acaaatacca    3600

aaaatcttca caaacgtggg cttccgatat cacctggaga gccccatcag ttcatcgcag    3660

aggcgcgagg acgatcgcat cacctacatc aacaagggtc aattctatgg aataacgctg    3720

gagtatgtgc acgatgcgga aaagcccatt aagaacacca ccgtcaagag tgtgatcatg    3780
```

```
ctaatgttcc gcgaggagaa gagtcccgag gatgagatca aggcctggca attctggcac    3840

agtcgtcagc attccgtgaa gcagagaatc ttggatgcag atacgaagaa ctcggttggc    3900

ctcgttggct gcatcgagga agtgtcgcac aatgccatcg ccgtctactg gaatccgctg    3960

gagagctccg ccaagatcaa cattgcggtt cagtgcttga gcacggattt cagcagtcaa    4020

aagggaggcc tgccgctgca cgtacaaatc gacacatttg aggaccccag agatacggcg    4080

gtcttccacc gcggctactg tcagataaag gtcttctgcg ataagggcgc cgaacgaaag    4140

acgcgcgatg aagagcggcg ggccgccaaa cgaaagatga cagccacggg cagaaagaag    4200

ctggacgagc tttaccatcc ggtaacggat cggtccgagt tctatggcat gcaggacttc    4260

gccaagccgc cggtgctatt ctcgcccgcc gaggacatgg agaagagctt ctacggccat    4320

gagactgact cgccggacct gaaggggggcc tcaccgttcc tgctccacgg ccagaaggtg    4380

gccacgccga cgctcaagtt ccacaaccat tttccgcccg acatgcagac cgataagaag    4440

gatcacatac tggaccagaa catgttgacc agcacacccc tgaccgactt tggtccgccg    4500

atgaagcgcg gcaggatgac gccgccgacc tcggaacgcg tgatgctgta cgtgcggcag    4560

gagaacgagg aggtgtatac accgttgcac gtggtgccgc ccaccacgat cggcctgcta    4620

aatgcgattg aaaacaaata caaaatctca acaacgagca taaataacat ttatcgcaca    4680

aacaagaagg ggattactgc gaaaattgac gatgacatga tatcgttcta ctgcaacgag    4740

gacatctttc tgctggaggt gcaacagatc gaggacgacc tgtacgatgt gacgctcacg    4800

gagctgccca tcagtagcg ctggcagtac gggtagcacc cgctaaccgc actcaaaaaa    4860

aaaagcaaac aaacacacaa attacggaca caacaagttg tttcaataag ccattttcca    4920

tagagcctaa gtctaaatat cgtagttata ataatgggat ccgcaacaaa tcgagttgca    4980

acgaatgtta agaacgctaa cacaatacgc atgtaaaatg atactttaaa attgatttag    5040

ttattttagc aacaatgaga ttatctaaaa ttgtttgatc aaattttaca ttctcgctat    5100

gtctatagat aattctaagc ccgtaagccc ataagcgtaa tcgtaatcgt aatcgtaccg    5160

tgtatttatg ctcatatata aacaactata tatatatata tatatatata tatgtgcgga    5220

gtgcaacagt gtctgtccag taggagataa gtctcgtttc cgctcccctg cttatgctat    5280

gaccttaggt ccagggcaag tatgagttac cgaatctatc tattaggtgc atctaacgaa    5340

aggaatcatt agctctgcac gaactctagc cgtagcctat tgtaatccat ttgtatgttt    5400

ggcttaagcg ttttacttgt tgaatataaa gtgtaaaatt atttttgaaa aaaaaaaacc    5460

cacacaaaac acaaatcgtt tgttctatat ttctgtttca aaactaactc gttacccaca    5520

atcccctctg ttatgtataa ttaggatctc tgtacac                             5557
```

<210>   39

<211> 1331
<212> PRT
<213> Drosophila

<400> 39

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1   5   10   15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20   25   30

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
        35   40   45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50   55   60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65   70   75   80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
            85   90   95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
            100   105   110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115   120   125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
            165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
            180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
        195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
210   215   220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met

225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
             245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
             260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
             275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
             290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
             325   330   335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
             340   345   350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
             355   360   365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
             370   375   380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385   390   395   400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
             405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
             420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
             435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
             450   455   460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
        485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
        500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
        515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
    530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545   550   555   560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
        565   570   575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
        580   585   590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
        595   600   605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
    610   615   620

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
625   630   635   640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
            645   650   655

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
        660   665   670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
        675   680   685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
    690   695   700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705   710   715   720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
            725   730   735

Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln Gln
        740   745   750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln His His Gln
        755   760   765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
      770   775   780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785   790   795   800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
        805   810   815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
        820   825   830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
        835   840   845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
    850   855   860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865   870   875   880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys
        885   890   895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
        900   905   910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
        915   920   925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
      930   935   940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
945   950   955   960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
        965   970   975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
        980   985   990

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
      995   1000   1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
     1010   1015   1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
     1025   1030   1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
     1040   1045   1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
     1055   1060   1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
     1070   1075   1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
     1085   1090   1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
     1100   1105   1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
     1115   1120   1125

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
     1130   1135   1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
     1145   1150   1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
     1160   1165   1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
     1175   1180   1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
     1190   1195   1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
     1205   1210   1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn
    1235   1240   1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile
    1250   1255   1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
    1265   1270   1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
    1280   1285   1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
    1295   1300   1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
    1310   1315   1320

Thr Leu Thr Glu Leu Pro Asn Gln
    1325   1330

<210>   40
<211>   18
<212>   DNA
<213>   murine

<400>   40
ggatcagaag accatgcc   18

<210>   41
<211>   18
<212>   DNA
<213>   murine

<400>   41
aggctgttag agttggtg   18

<210>   42
<211>   18
<212>   DNA
<213>   murine

<400>   42
ctgtagccag ctttcatc   18

<210>   43
<211>   19
<212>   DNA
<213>   murine

<400> 43
gctggtgaaa aggacctct   19

<210> 44
<211> 20
<212> DNA
<213> murine

<400> 44
cacaggacta gaacacctgc   20

<210> 45
<211> 17
<212> DNA
<213> murine

<400> 45
cacattgaag aggtggc   17

<210> 46
<211> 20
<212> DNA
<213> MURINE

<400> 46
aagggtgagc aggttcgctt   20